Claims as Pending after Preliminary Amendment

1. An isolated, purified, or recombinant polynucleotide comprising a contiguous span of at least 12 nucleotides of SEQ ID Nos 1 to 4, 6 and 31, or the complements thereof, wherein said contiguous span comprises:

- at least one of the following nucleotide positions of SEQ ID No 1: 1 to 3585 and 4644 to 5222; and/or
- at least one of the following nucleotide positions of SEQ ID No 2: 1 to 16155 and 16331 to 21278; and/or
- at least one of the following nucleotide positions of SEQ ID No 3: 1 to 5531 and 6355 to 21636; and/or
- at least one of the following nucleotide positions of SEQ ID No 4: 1 to 519 and 2563 to 5566; and/or
- at least one of the following nucleotide positions of SEQ ID No 6: 1 to 1791.

2. An isolated, purified, or recombinant polynucleotide comprising a contiguous span of at least 12 nucleotides of SEQ ID No 31, or the complements thereof, wherein said contiguous span comprises at least one of the following nucleotide positions of SEQ ID No 31: 1 to 480 and 717 to 983.

3. An isolated, purified, or recombinant polynucleotide consisting essentially of a contiguous span of 8 to 50 nucleotides of anyone of SEQ ID Nos 1 to 3 and 32 to 69 or the complement thereof, wherein said span includes a *G713 or 13q31-q33*-related biallelic marker in said sequence.

4. A polynucleotide according to claim 3, wherein said *G713 or 13q31-q33*-related biallelic marker is selected from the group consisting of A1 to A49, and the complements thereof.

5. A polynucleotide according to claim 3, wherein said *13q31-q33*-related biallelic marker is selected from the group consisting of A16 to A20 and the complements thereof.

8. A polynucleotide according to claim 6, wherein said polynucleotide consists essentially of a sequence selected from the following sequences: P1 to P49, and the complementary sequences thereto.

11. The polynucleotide of claim 3 consisting essentially of a contiguous span of 8 to 50 nucleotides of anyone of SEQ ID Nos 1 to 3 and 32 to 69 or the complement thereof, wherein the 3' end of said contiguous span is located at the 3' end of said polynucleotide, and wherein the 3' end of said polynucleotide is located within 20 nucleotides upstream of a *G713 or 13q31-q33*-related biallelic marker in said sequence.

A1

13. A polynucleotide according to claim 11, wherein said polynucleotide consists essentially of a sequence selected from the following sequences: D1 to D49, and E1 to E49.

A2

14. An isolated, purified, or recombinant polynucleotide consisting essentially of a sequence selected from the following sequences: B1 to B49 and C1 to C49.

15. An isolated, purified, or recombinant polynucleotide which encodes a polypeptide comprising a contiguous span of at least 6 amino acids of SEQ ID Nos 5 or 7.

19. A polynucleotide according to any one of claims 1, 2 or 3 attached to a solid support.

A3

23. A recombinant vector comprising a polynucleotide according to claim 1.

A4

24. A host cell comprising a recombinant vector according to claim 23.

25. A non-human host animal or mammal comprising a recombinant vector according to claim 23.

28. A method of genotyping comprising determining the identity of a nucleotide at a *G713- or 13q31-q33*-related biallelic marker or the complement thereof in a biological sample.

35. A method of estimating the frequency of an allele of a *G713- or 13q31-q33*-related biallelic marker in a population comprising:

a) genotyping individuals from said population for said biallelic marker according to the method of claim 28; and

b) determining the proportional representation of said biallelic marker in said population.

36. A method of detecting an association between a genotype and a trait, comprising the steps of:

a) determining the frequency of at least one *G713- or 13q31-q33*-related biallelic marker in trait positive population according to the method of claim 35;

b) determining the frequency of at least one *G713- or 13q31-q33*-related biallelic marker in a control population according to the method of claim 35; and

c) determining whether a statistically significant association exists between said genotype and said trait.

37. A method of estimating the frequency of a haplotype for a set of biallelic markers in a population, comprising:

a) genotyping at least one *G713- or 13q31-q33*-related biallelic marker according to claim 28 for each individual in said population;

b) genotyping a second biallelic marker by determining the identity of the nucleotides at said second biallelic marker for both copies of said second biallelic marker present in the genome of each individual in said population; and

c) applying a haplotype determination method to the identities of the nucleotides determined in steps a) and b) to obtain an estimate of said frequency.

39. A method of detecting an association between a haplotype and a trait, comprising the steps of:

a) estimating the frequency of at least one haplotype in a trait positive population according to the method of claim 37;

b) estimating the frequency of said haplotype in a control population according to the method of claim 37; and

c) determining whether a statistically significant association exists between said haplotype and said trait.

47. A method of determining whether an individual is at risk of developing schizophrenia, comprising:

a) genotyping at least one *13q31-q33*-related biallelic marker according to the method of claim 30; and

b) correlating the result of step a) with a risk of developing schizophrenia.

48. A method according to claim 47 wherein said *13q31-q33*-related biallelic marker is selected from the group consisting of A12 to A49 and the complements thereof.

51. A computer readable medium having stored thereon a sequence selected from the group consisting of a nucleic acid code comprising one of the following:

a) the polynucleotide of claim 1;

b) a contiguous span of at least 12 nucleotides of SEQ ID No 31 or the complements thereof, wherein said contiguous span comprises at least one of the following nucleotide positions: 1 to 480 and 717 to 983 of SEQ ID No 31;

c) a contiguous span of at least 12 nucleotides of SEQ ID No 4 or the complements thereof, wherein said contiguous span comprises at least one of the following nucleotide positions: 1 to 519 and 2563 to 5566 of SEQ ID No 4;

d) a contiguous span of at least 12 nucleotides of SEQ ID No 6 or the complements thereof;

e) a contiguous span of at least 12 nucleotides of at least one of SEQ ID Nos 32 to 69, or the complements thereof; and

f) a nucleotide sequence complementary to any one of the preceding nucleotide sequences.

57. A method for comparing a first sequence to a reference sequence, comprising the steps of:

reading said first sequence and said reference sequence through use of a computer program which compares sequences; and

determining differences between said first sequence and said reference sequence with said computer program,

wherein said first sequence is selected from the group consisting of a nucleic acid code comprising one of the following:

a) the polynucleotide of claim 1;

b) a contiguous span of at least 12 nucleotides of SEQ ID No 31 or the complements thereof, wherein said contiguous span comprises at least one of the following nucleotide positions: 1 to 480 and 717 to 983 of SEQ ID No 31;

c) a contiguous span of at least 12 nucleotides of SEQ ID No 4 or the complements thereof, wherein said contiguous span comprises at least one of the following nucleotide positions: 1 to 519 and 2563 to 5566 of SEQ ID No 4;

h) a contiguous span of at least 12 nucleotides of SEQ ID No 6 or the complements thereof;

i) a contiguous span of at least 12 nucleotides of at least one of SEQ ID Nos 32 to 69, or the complements thereof;

f) a nucleotide sequence complementary to any one of the preceding nucleotide sequences; and

a polypeptide code comprising a contiguous span of at least 6 amino acids of SEQ ID Nos 5 or 7.